III. REMARKS

Claims 1, 3-4, 7-12, 14-15, 17-18, and 20-23 are pending in this application. By this Amendment, claims 1, 3-4, 7-8, 14, 17, and 20 have been amended, claims 21-23 are newly presented, and claims 2, 5-6, 13, 16, and 19 have been cancelled. Applicants do not acquiesce in the correctness of the rejections, and do not concede that any claim is not patentable over the art cited by the Examiner. The present claim amendments and cancellations are only for facilitating expeditious prosecution of the claimed subject matter. Applicants respectfully reserve the right to pursue these and other claims in one or more continuation and/or divisional patent applications. Reconsideration in view of the following remarks is respectfully requested.

Rejections under 35 U.S.C. § 103(a)

In the Office Action of January 27, 2009 (hereinafter, "the Office Action"), claims 1-4, 6-8, 10-12, 14, 15, 17, 18, and 20 are rejected under 35 U.S.C. § 103(a) as being unpatentable over Rungsarityotin *et al.* (Wasinee Rungsarityotin *et al.*, *Grid computing and bioinformatics development. A case study on the* Oryza sativa *(rice) genome*, 74 PURE APPL. CHEM. 891-97 (2002) (hereinafter, "Rungsarityotin")) in view of Patten *et al.* (US Pat. 6,531,316 B1, hereinafter, "Patten"), with additional support from the Merriam-Webster online dictionary ("encrypt," "encode," "encipher," and "cipher"); and claims 5, 13, 16, and 19 are rejected under 35 U.S.C. § 103(a) as being unpatentable over Rungsarityotin in view of Patten and Jorgenson *et al.* (US Pub. No. 2004/0221163 A1, hereinafter, "Jorgenson"), with additional support from the Merriam-Webster online dictionary.

With regard to independent claim 1, Applicants have amended this claim herein to provide improved clarity with regard to the features which distinguish the claim from the cited

art, and respectfully submit that the combination of Rungsarityotin, Patten, and the Merriam-Webster online dictionary does not teach or suggest a computer-implemented security system for securing an electronic version of a nucleotide chain sequence, including each and every feature claimed herein.

For example, Applicants submit that the combination of Rungsarityotin and Patten do not teach the amended feature of "regenerating the nucleotide chain from the decrypted sequence of the at least one exon and the unencrypted sequence of the at least one intron *to re-form the original nucleotide chain sequence*" (claim 1, lines 25-27). No new matter is added by this amendment, as support may be found in previously presented claim 6 (now cancelled) as well as p. 7, lines 16-17.

In the Office Action, the Office relies on Patten at col. 23, 3rd and 4th paragraphs, to allegedly teach the "regenerating" feature (Office Action, p. 5, first full paragraph). As discussed relative to a similarly claimed feature in the Amendment of October 30, 2008, however, rather than teaching *regenerating an original nucleotide chain sequence*, the cited passage in Patten teaches use of "several different general classes of *sequence modification methods, such as mutation, recombination*, etc." (col. 21, lines 66-67). Among these *sequence modification methods* are methods such as in vitro recombination of nucleic acids (col. 22, line 22 *et seq.*); recursive recombination of nucleic acids in vivo (col. 22, line 39 *et seq.*); whole genome recombination methods in which whole genomes of cells or other organisms are combined (col. 22, line 51 *et seq.*); synthetic recombination methods (in which oligonucleotides corresponding to targets of interest are synthesized and reassembled in PCR or ligation reactions) (col. 23, line 4 *et seq.*); and in silico methods of recombination in which genetic algorithms are used to

recombine sequence strings which correspond to homologous (or non-homologous) nucleic acids[1] resulting in recombined sequence strings (col. 23, line 32 *et seq.*). Applicants respectfully emphasize that modification of a genetic sequence through any of the aforementioned methods taught by Patten will result in the generation of a new and different genetic sequence -- not *the original nucleotide sequence*, as claimed in claim 1.

Specifically, Patten's "in silico methods of recombination," cited by the Office, result in recombined strings, which in turn produce random, partially random, or designed variants (col. 23, line 32 *et seq.*). As is well known in the art, and as has been known since well before instant application's filing date of April 1, 2004, genetic recombination is a specific process by which a strand of DNA or RNA is broken and subsequently joined to a different DNA molecule, frequently occurring during eukaryotic meiosis as chromosomal crossover between paired chromosomes. The resulting offspring from the crossover have combinations of genes which differ from both parents. Accordingly, recombination, as it is understood in the art and taught by Patten, does not teach or suggest the feature of "*regenerating* the nucleotide chain ... to *re-form the original nucleotide chain sequence*" (claim 1, lines 25-27).

In a separate passage of the Office Action, the Office also appears to assert that Rungsarityotin's teaching of "choosing between textual and graphical output and transforming XML documents to scalable vector graphics (Figure 2 caption) ... represents ... regeneration." (Office Action, p. 5, in the paragraph continuing from p. 4.) Applicants respectfully submit, as above, that the current amendment to the "regenerating" feature provides improved clarity with regard to this feature, and further maintain that, for reasons discussed in

[1] A substantially homologous nucleic acid sequence is a sequence which can be transcribed and/or translated to provide an amino acid sequence which is substantially homologous.

the Amendment of January 29, 2008, Rungsarityotin does not disclose regenerating "the original nucleotide chain sequence." Particularly, because Rungsarityotin uses a line to represent the non-coding regions of the rice genome segment (FIG. 2), the output data is incomplete in that it does not include the nucleotide chain sequence of the introns; accordingly, it would not be possible to regenerate the original nucleotide chain sequence based on Rungsarityotin's teachings.

With regard to the "selectively encrypting" feature of claim 1, Applicants have amended this feature herein to recite "selectively encrypting the sequence of only the at least one exon identified in the nucleotide chain to provide security over a network, wherein the selectively encrypting only the sequence of the at least one exon utilizes cipher block chain encrypting" (claim 1, lines 10-13). No new matter is added by this amendment, as this feature was previously recited in claim 5 (now cancelled).

In the Office Action, the Office relies on Rungsarityotin at FIG. 2 and pp. 892 and 894 to teach the "selectively encrypting" feature. In these passages, Rungsarityotin teaches "using expressed sequence tags (ESTs) treated as genes and marker names (i.e. AP002882 and RZ69) (citation omitted) along the sequence with non-coding regions merely listed as a line (Figure 2) and providing security over a network" (Office Action, p. 4). The Office further relies on Jorgenson at the abstract; claims 1, 14, 48, and 58; and paragraphs [0033], [0058], and [0119] to teach "securing transmitting data using an encryption scheme including information from DNA tests" including "cipher block chaining" (Office Action, p. 11).

Jorgenson teaches methods for improving access control, administrative monitoring, reliability, and flexibility for data transmission and remote application sharing over a network

(abstract), wherein the network may employ a variety of authentication and encryption means which may include, e.g., cipher block chaining ([0119]). In [0024], Jorgenson describes an embodiment in which the authentication and encryption scheme includes:

> (a) a request being caused to forward from the intelligent data carrier to the network server that the intelligent data carrier be authenticated;
>
> (b) the network server presenting to the intelligent data carrier a plurality of authentication methods;
>
> (c) the intelligent data carrier selecting one authentication method from the plurality through an event;
>
> (d) the network server sending the intelligent data carrier a demand, based on the selected method, for authentication data from the intelligent data carrier;
>
> (e) the network server transforming the authentication data received from the intelligent data carrier into one or more data authentication objects, *wherein each data authentication object is a data vector object, capable of being analyzed using one or more classifiers*;
>
> (f) the network server analyzing the data authentication objects, according to the one or more classifiers, thereby determining the result of the authentication; and
>
> (g) the network server sending the result to the intelligent data carrier, indicating a successful or failed authentication attempt (emphasis added).

In paragraph [0031], the one or more classifiers in step e) comprise a super classifier derived from the more than one data vector objects, the super classifier being based on physical biometrics, which may include, among other tests, DNA tests, retinal or iris scan, etc. ([0032]). Thus, in contrast with the Office's characterization that Jorgenson teaches "securing transmitting data using an encryption scheme including information from DNA tests" including "cipher block chaining" (Office Action, p. 11), Jorgenson in fact teaches authentication of a data carrier through use of *a data vector object, capable of being analyzed using one or more classifiers, a plurality of which may comprise a super classifier, which may be based on DNA tests, among other physical biometrics.* Jorgenson does not teach encryption *of* DNA data through cipher

block chaining or any other type of encryption. Jorgenson teaches the use of DNA tests to ultimately aid in the authentication of a data carrier. Therefore, Applicants submit that Jorgenson's teachings are not relevant to those of Rungsarityotin's use of expressed sequence tags (ESTs) as candidate genes along the sequence with non-coding regions merely listed as a line.

With regard to the feature of "identifying a sequence of at least one exon and a sequence of at least one intron in the nucleotide chain sequence" (claim 1, lines 8-9), Applicants maintain that the proposed combination of Rungsarityotin and Patten fails to teach or suggest the computer-implemented security system of claim 1 including this feature. The Office maintains in the current Office Action that this feature is taught by Rungsarityotin at p. 894, first paragraph and the abstract. Applicants respectfully reiterate the position presented in the Amendment of June 23, 2008, that the cited teachings of Rungsarityotin all differ from the claimed "identifying a sequence of at least one exon and a sequence of at least one intron in the nucleotide chain sequence." For example, Rungsarityotin's "exchanging information on a particular gene or coding regions" (Office Action, pp. 3-4) differs from the claimed "identifying" feature because, among other reasons, it fails to discuss introns at all, much less *identifying a sequence of at least one intron*. Further, Rungsarityotin's "integrating a physical map of BAC sequence from a rice chromosome (citation omitted), using BAC-end sequences and BAC fingerprint contigs and linking critical regions of interest onto a sequence-ready map" (Office Action, p. 4) differs from the claimed "identifying" feature because, among other reasons, expressed sequence tags and bacteria artificial clones are artificial constructs which do not comprise "least a portion of a

genome of an organism" (claim 1, lines 2-3), much less a specific portion of an organism's genome, e.g., an intron.

Although the Office has repeated its position that the aforementioned features of Rungsarityotin "represent" *identifying a sequence of at least one exon and a sequence of at least one intron in the nucleotide chain sequence* in successive Office Actions, Applicants respectfully request that the Office provide additional explanation or clarification as to how Rungsarityotin's features allegedly accomplish this representation. In the absence of such clarification, Applicants maintain for the reasons given above that it does not.

With regard to the feature of "outputting the ... the nucleotide chain sequence, including ... the unencrypted sequence of the at least one intron" (claim 1, lines 14-16), Applicants further maintain that the proposed combination of Rungsarityotin and Patten fails to teach or suggest this feature. In the current Office Action, the Office admits that Rungsarityotin does not teach this feature, and maintains its reliance on Patten at col. 22, lines 9-22 to teach this feature (Office Action, p. 5). As discussed in the Amendment of October 30, 2008, however, the cited passage exhaustively recites,

> ...unencrypted nucleic acids that comprise split gene sequences, trans-splicing introns, toxic genetic elements, or the like are optionally modified to improve, e.g., splicing or activity according to any of these techniques or combinations of these techniques. Furthermore, nucleic acid sequences to be modified are optionally derived from various known or designed genetic elements available, e.g., from many public databases, such as Genbank(R). The following exemplify some of the different types of preferred formats for diversity generation in the context of the present invention, including, e.g., certain recombination based diversity generation formats. (Col. 22, lines 9-22.)

The only reference to "introns" at all is to "trans-splicing introns." As is known in the art, and has been known since prior to the April 1, 2004 filing date of the instant application, trans-splicing is a specific type of RNA processing in eukaryotic cells in which nucleotide sequences from two different primary RNA transcripts are joined end to end and are ligated, or joined by a ligase, which is an enzyme that catalyzes the joining of two large molecules by forming a new chemical bond, usually by hydrolysis of a small chemical group pendant to one of the now-joined larger molecules. Trans-splicing results in an RNA transcript that can be used for molecular therapy to address mutated gene products, and can be contrasted with cis-splicing, in which a single molecule is processed at a time.

Thus, the cited passage is not relevant to encryption, and does not teach "the unencrypted sequence of the at least one intron" as claimed. Additional passages in Patten which discuss the use of introns also fail to teach "the unencrypted sequence of the at least one intron" as discussed previously in the Amendment of October 30, 2008. Applicants further reiterate the arguments in the Amendment of October 30, 2008, elaborating on Applicants' position that "encryption" as contemplated by Patten is wholly inapposite to the "encryption," and therefore to the "unencrypted introns," of the claimed invention.

Applicants have further amended claim 1 to include the features of "on a first application, identifying ...; selectively encrypting ...; [and] outputting," and "on a second application, receiving ...; decrypting ...; and regenerating" (claim 1, lines 7-25). No new matter is added by these amendments, as support for the first application and second application features may be found in the specification in at least p. 4, lines 13-14, and FIG. 1, specifically bioinformatics applications 10 and 20, respectively. Applicants have further amended claim 1 to include the

features of "transmitting the ... sequence" (claim 1, lines 19-20), "receiving the ... sequence" (claim 1, lines 22-23), and "decrypting the encrypted sequence" (claim 1, line 24). No new matter is added by these amendments, as the transmitting feature was previously recited in claim 2, and the receiving and decrypting features were previously recited in claim 6. Both of claims 2 and 6 are cancelled herein.

On the basis of at least the amendments contained herein and the above remarks, Applicants submit that the combination of Patten and Rungsarityotin, with support from Merriam Webster, do not teach each and every feature recited herein. In view of the above-noted deficiencies, Applicants respectfully request withdrawal of the rejection under § 103(a).

With respect to the rejections of independent claims 8, 14, and 17 under § 103(a), Applicants note that each claim includes features similar in scope to those already addressed above with respect to claim 1, and has been amended analogously herein. Further, the Office relies on the same arguments and interpretations of Rungsarityotin, Patten, and the Merriam-Webster Online Dictionary as discussed above with respect to claim 1. To this extent, Applicants herein incorporate the arguments presented above with respect to claim 1, and respectfully request withdrawal of the rejections of claims 8, 14, and 17 for the above-stated reasons. Accordingly, Applicants respectfully request that the rejections to independent claims 1, 8, 14, and 17 be withdrawn.

With respect to dependent claim 3, Applicants have amended this claim herein to recite the "computer-implemented security system of claim 1, wherein the transmitting includes packaging the encrypted sequence of the at least one exon and the unencrypted sequence of the at least one intron into at least one XML document." Support for this amendment may be found in

the specification in at least p. 4, lines 20-22, and p. 6, lines 7-9. Claim 3 has further been amended to maintain proper dependency in view of the cancellation of claim 2 herein.

With respect to dependent claim 4, Applicants have similarly amended this claim herein to maintain proper dependency in view of the current cancellation of claim 2.

With respect to dependent claim 7, Applicants have amended this claim herein to recite "computer-implemented security system of claim 1, wherein the receiving comprises receiving the encrypted sequence of the at least one exon and the unencrypted sequence of the at least one intron into a bioinformatics database for receiving nucleotide chain queries." Support for this amendment may be found in the specification in at least p. 4, lines 18-19. Claim 7 has further been amended to maintain proper dependency in view of the cancellation of claim 6 herein.

The above-described amendments to claims 3, 4, and 7 are intended to provide improved clarity with regard to the claimed invention. With respect to dependent claims 3, 4, 7, 10-12, 15, and 18, and 20, and with further respect to dependent claims 3, 4, and 7, Applicants respectfully submit that these claims are allowable for reasons stated above relative to independent claims 1, 8, 14, and 17, as well as for their own additional claimed subject matter. Accordingly, Applicants respectfully request that the Office withdraw the rejections under 35 U.S.C. § 103(a) to claims 3, 4, 7, 10-12, 15, and 18, and 20.

With respect to new dependent claims 21-23, Applicants submit that these claims are also allowable for reasons stated above relative to independent claims 1 and 8, as well as for their own additional claimed subject matter. No new subject matter is added by the recitation of these claims, as support can be found for new claims 21 and 23 in the specification at p. 6, lines 14-15, and for new claim 22 at p. 6, lines 7-11. Further, no additional fees are due, as the number of

pending claims does not exceed the number of claims pending as of the filing date of the application.

IV. CONCLUSION

Applicants respectfully submit that the Application as presented is in condition for allowance. Should the Examiner believe that anything further is necessary in order to place the application in better condition for allowance, the Examiner is requested to contact Applicants' undersigned attorney at the telephone number listed below.

Respectfully submitted,

/Jayme M. Torelli/
Jayme M. Torelli
Reg. No. 62,735

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Hoffman Warnick LLC
75 State Street, 14th Floor
Albany, New York 12207
Phone: (518) 449-0044
Fax: (518) 449-0047